

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 11:44:09 ; Search time 164 Seconds
(without alignments)
551.801 Million cell updates/sec

Title: US-10-694-978-2
Perfect score: 218
Sequence: 1 MSFVGENSGVKGSEDMEND.....IEFSFQVCKRAEMSPSEVSD 218

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1846076 seqs, 415116000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database :

- Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCr_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/PCrUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US10A_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	218	100.0	218 15 US-10-695-195-2	Sequence 2, Appl1
2	218	100.0	218 15 US-10-694-978-2	Sequence 2, Appl1
3	65	29.8	176 9 US-09-965-528-25	Sequence 25, Appl1
4	65	29.8	176 11 US-09-969-984-25	Sequence 25, Appl1
5	55	25.2	115 13 US-10-095-407-5	Sequence 9, Appl1
6	55	25.2	115 13 US-10-095-407-9	Sequence 9, Appl1
7	55	25.2	115 13 US-10-095-407-13	Sequence 13, Appl1
8	55	25.2	136 13 US-10-095-407-11	Sequence 11, Appl1
9	55	25.2	157 14 US-09-876-790-10	Sequence 10, Appl1
10	55	25.2	157 14 US-10-302-554-9	Sequence 9, Appl1
11	55	25.2	157 14 US-10-302-554-15	Sequence 15, Appl1

12	55	25.2	157 16 US-10-888-918-10	Sequence 10, Appl1
13	55	25.2	157 17 US-10-888-867-10	Sequence 10, Appl1
14	55	25.2	157 17 US-10-888-779-10	Sequence 10, Appl1
15	55	25.2	157 17 US-10-888-780-10	Sequence 10, Appl1
16	55	25.2	157 17 US-10-888-931-10	Sequence 10, Appl1
17	55	25.2	167 13 US-10-095-407-7	Sequence 7, Appl1
18	55	25.2	178 13 US-10-095-407-2	Sequence 11, Appl1
19	55	25.2	178 14 US-10-139-833-11	Sequence 3, Appl1
20	55	25.2	192 10 US-09-876-790-3	Sequence 13, Appl1
21	55	25.2	192 14 US-10-139-833-13	Sequence 3, Appl1
22	55	25.2	192 16 US-10-888-918-3	Sequence 3, Appl1
23	55	25.2	192 17 US-10-888-867-3	Sequence 3, Appl1
24	55	25.2	192 17 US-10-888-779-3	Sequence 3, Appl1
25	55	25.2	192 17 US-10-888-780-3	Sequence 3, Appl1
26	55	25.2	192 17 US-10-888-931-3	Sequence 3, Appl1
27	55	25.2	193 13 US-10-063-867-142	Sequence 142, App
28	55	25.2	193 13 US-10-063-547-142	Sequence 142, App
29	55	25.2	193 13 US-10-063-551-142	Sequence 142, App
30	55	25.2	193 14 US-10-063-616-142	Sequence 142, App
31	55	25.2	193 14 US-10-063-569-142	Sequence 142, App
32	55	25.2	193 14 US-10-063-513-142	Sequence 142, App
33	55	25.2	193 14 US-10-063-515-142	Sequence 142, App
34	55	25.2	193 14 US-10-063-512-142	Sequence 142, App
35	55	25.2	193 14 US-10-063-502-142	Sequence 142, App
36	55	25.2	193 14 US-10-063-549-142	Sequence 142, App
37	55	25.2	193 14 US-10-063-554-142	Sequence 142, App
38	55	25.2	193 14 US-10-063-553-142	Sequence 142, App
39	55	25.2	193 14 US-10-063-518-142	Sequence 142, App
40	55	25.2	193 14 US-10-063-598-142	Sequence 142, App
41	55	25.2	193 14 US-10-227-693-142	Sequence 142, App
42	55	25.2	193 14 US-10-063-585-142	Sequence 142, App
43	55	25.2	193 14 US-10-063-588-142	Sequence 142, App
44	55	25.2	193 14 US-10-063-555-142	Sequence 142, App
45	55	25.2	193 14 US-10-063-554-142	Sequence 142, App
46	55	25.2	193 14 US-10-063-587-142	Sequence 142, App
47	55	25.2	193 14 US-10-063-538-142	Sequence 142, App
48	55	25.2	193 14 US-10-063-599-142	Sequence 142, App
49	55	25.2	193 14 US-10-063-580-142	Sequence 142, App
50	55	25.2	193 14 US-10-063-557-142	Sequence 142, App
51	55	25.2	193 14 US-10-063-585-142	Sequence 142, App
52	55	25.2	193 14 US-10-063-588-142	Sequence 142, App
53	55	25.2	193 14 US-10-063-735-142	Sequence 142, App
54	55	25.2	193 14 US-10-063-526-142	Sequence 142, App
55	55	25.2	193 14 US-10-063-586-142	Sequence 142, App
56	55	25.2	193 14 US-10-063-586-142	Sequence 142, App
57	55	25.2	193 14 US-10-063-546-142	Sequence 142, App
58	55	25.2	193 14 US-10-063-564-142	Sequence 142, App
59	55	25.2	193 14 US-10-063-662-142	Sequence 142, App
60	55	25.2	193 14 US-10-063-619-142	Sequence 142, App
61	55	25.2	193 14 US-10-063-669-142	Sequence 142, App
62	55	25.2	193 14 US-10-063-670-142	Sequence 142, App
63	55	25.2	193 14 US-10-063-671-142	Sequence 142, App
64	55	25.2	193 14 US-10-063-674-142	Sequence 142, App
65	55	25.2	193 14 US-10-063-675-142	Sequence 142, App
66	55	25.2	193 14 US-10-063-676-142	Sequence 142, App
67	55	25.2	193 14 US-10-063-686-142	Sequence 142, App
68	55	25.2	193 14 US-10-063-689-142	Sequence 142, App
69	55	25.2	193 14 US-10-063-692-142	Sequence 142, App
70	55	25.2	193 14 US-10-063-693-142	Sequence 142, App
71	55	25.2	193 14 US-10-063-694-142	Sequence 142, App
72	55	25.2	193 14 US-10-063-698-142	Sequence 142, App
73	55	25.2	193 14 US-10-063-699-142	Sequence 142, App
74	55	25.2	193 14 US-10-063-702-142	Sequence 142, App
75	55	25.2	193 14 US-10-063-705-142	Sequence 142, App
76	55	25.2	193 14 US-10-063-707-142	Sequence 142, App
77	55	25.2	193 14 US-10-063-709-142	Sequence 142, App
78	55	25.2	193 14 US-10-063-713-142	Sequence 142, App
79	55	25.2	193 14 US-10-063-724-142	Sequence 142, App
80	55	25.2	193 14 US-10-063-727-142	Sequence 142, App
81	55	25.2	193 14 US-10-063-730-142	Sequence 142, App
82	55	25.2	193 14 US-10-063-734-142	Sequence 142, App
83	55	25.2	193 14 US-10-063-736-142	Sequence 142, App
84	55	25.2	193 14 US-10-063-742-142	Sequence 142, App
85	55	25.2	193 14 US-10-063-743-142	Sequence 142, App

85	55	25.2	193	14	US-10-063-744-142	Sequence 142, App
86	55	25.2	193	14	US-10-063-565-142	Sequence 142, App
87	55	25.2	193	14	US-10-063-577-142	Sequence 142, App
88	55	25.2	193	14	US-10-063-591-142	Sequence 142, App
89	55	25.2	193	14	US-10-063-610-142	Sequence 142, App
90	55	25.2	193	14	US-10-063-673-142	Sequence 142, App
91	55	25.2	193	14	US-10-063-710-142	Sequence 142, App
92	55	25.2	193	14	US-10-063-711-142	Sequence 142, App
93	55	25.2	193	14	US-10-063-712-142	Sequence 142, App
94	55	25.2	193	14	US-10-063-714-142	Sequence 142, App
95	55	25.2	193	14	US-10-063-715-142	Sequence 142, App
96	55	25.2	193	14	US-10-063-716-142	Sequence 142, App
97	55	25.2	193	14	US-10-063-717-142	Sequence 142, App
98	55	25.2	193	14	US-10-063-720-142	Sequence 142, App
99	55	25.2	193	14	US-10-063-722-142	Sequence 142, App
100	55	25.2	193	14	US-10-063-726-142	Sequence 142, App
101	55	25.2	193	14	US-10-063-728-142	Sequence 142, App
102	55	25.2	193	14	US-10-063-731-142	Sequence 142, App
103	55	25.2	193	14	US-10-063-732-142	Sequence 142, App
104	55	25.2	193	14	US-10-063-523-142	Sequence 142, App
105	55	25.2	193	14	US-10-063-527-142	Sequence 142, App
106	55	25.2	193	14	US-10-063-529-142	Sequence 142, App
107	55	25.2	193	14	US-10-063-581-142	Sequence 142, App
108	55	25.2	193	14	US-10-063-583-142	Sequence 142, App
109	55	25.2	193	14	US-10-063-589-142	Sequence 142, App
110	55	25.2	193	14	US-10-063-593-142	Sequence 142, App
111	55	25.2	193	14	US-10-063-596-142	Sequence 142, App
112	55	25.2	193	14	US-10-063-600-142	Sequence 142, App
113	55	25.2	193	14	US-10-063-604-142	Sequence 142, App
114	55	25.2	193	14	US-10-063-607-142	Sequence 142, App
115	55	25.2	193	14	US-10-063-612-142	Sequence 142, App
116	55	25.2	193	14	US-10-063-615-142	Sequence 142, App
117	55	25.2	193	14	US-10-063-640-142	Sequence 142, App
118	55	25.2	193	14	US-10-063-642-142	Sequence 142, App
119	55	25.2	193	14	US-10-063-644-142	Sequence 142, App
120	55	25.2	193	14	US-10-063-649-142	Sequence 142, App
121	55	25.2	193	14	US-10-063-650-142	Sequence 142, App
122	55	25.2	193	14	US-10-063-652-142	Sequence 142, App
123	55	25.2	193	14	US-10-063-654-142	Sequence 142, App
124	55	25.2	193	14	US-10-063-659-142	Sequence 142, App
125	55	25.2	193	14	US-10-063-661-142	Sequence 142, App
126	55	25.2	193	14	US-10-063-528-142	Sequence 142, App
127	55	25.2	193	14	US-10-063-540-142	Sequence 142, App
128	55	25.2	193	14	US-10-063-568-142	Sequence 142, App
129	55	25.2	193	14	US-10-063-570-142	Sequence 142, App
130	55	25.2	193	14	US-10-063-582-142	Sequence 142, App
131	55	25.2	193	14	US-10-063-587-142	Sequence 142, App
132	55	25.2	193	14	US-10-063-592-142	Sequence 142, App
133	55	25.2	193	14	US-10-063-597-142	Sequence 142, App
134	55	25.2	193	14	US-10-063-602-142	Sequence 142, App
135	55	25.2	193	14	US-10-063-606-142	Sequence 142, App
136	55	25.2	193	14	US-10-063-609-142	Sequence 142, App
137	55	25.2	193	14	US-10-063-611-142	Sequence 142, App
138	55	25.2	193	14	US-10-063-614-142	Sequence 142, App
139	55	25.2	193	14	US-10-063-639-142	Sequence 142, App
140	55	25.2	193	14	US-10-063-643-142	Sequence 142, App
141	55	25.2	193	14	US-10-063-646-142	Sequence 142, App
142	55	25.2	193	14	US-10-063-651-142	Sequence 142, App
143	55	25.2	193	14	US-10-063-653-142	Sequence 142, App
144	55	25.2	193	14	US-10-063-660-142	Sequence 142, App
145	55	25.2	193	14	US-10-063-665-142	Sequence 142, App
146	55	25.2	193	14	US-10-063-584-142	Sequence 142, App
147	55	25.2	193	14	US-10-063-536-142	Sequence 142, App
148	55	25.2	193	14	US-10-063-562-142	Sequence 142, App
149	55	25.2	193	14	US-10-063-638-142	Sequence 142, App
150	55	25.2	193	14	US-10-063-666-142	Sequence 142, App

ALIGNMENTS

```
; Sequence 2, Application US/10695195
; Publication No. US20040068099A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/695,195
; FILING DATE: 27-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,412
; FILING DATE: 17-Sep-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0904K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-695-195-2

Query Match      100.0%; Score 218; DB 15; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.2e-199;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MSFVGENSGVKGWSEMEKDEPOCCLEDPAGSPLEBGPSPLEPTNNFVHTRKYVSLNPKKF 60
        |||
DB      1 MSFVGENSGVKGWSEMEKDEPOCCLEDPAGSPLEBGPSPLEPTNNFVHTRKYVSLNPKKF 60
        |||

QY      61 SHHDQHKVLDVDSGNLIVAPDKNYIRPEIFPALASLSSASAEKGSLLILGVSKGEFCL 120
        |||
DB      61 SHHDQHKVLDVDSGNLIVAPDKNYIRPEIFPALASLSSASAEKGSLLILGVSKGEFCL 120
        |||

QY      121 YCKKDGQGHSPISQLKKEKIMKLAOKESARRPFIYRAOVGSRNMLEAHPGWFICTS 180
        |||
DB      121 YCKKDGQGHSPISQLKKEKIMKLAOKESARRPFIYRAOVGSRNMLEAHPGWFICTS 180
        |||

QY      181 CNCNEPVGVTDKPENRKHIEFSFOPVCKAEMSPSEVSD 218
        |||
DB      181 CNCNEPVGVTDKPENRKHIEFSFOPVCKAEMSPSEVSD 218
        |||
```

```
RESULT 2
US-10-694-978-2
; Sequence 2, Application US/10694978
; Publication No. US2004008766A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
```

CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-694-978-2

Query Match 100.0%; Score 218; DB 15; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.2e-199; Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFVGENSGVGMSEDEKDEPOCCLEDPAGSPLEPPPSLPTMNFVTSRKVSLNPKKF 60
DB 1 MSFVGENSGVGMSEDEKDEPOCCLEDPAGSPLEPPPSLPTMNFVTSRKVSLNPKKF 60
QY 61 SHDQHKVLVDSGNLIAVPDKNYIRPEIFPALASSLSASAKGSLILLGVSKGEFCL 120
DB 61 SHDQHKVLVDSGNLIAVPDKNYIRPEIFPALASSLSASAKGSLILLGVSKGEFCL 120
QY 121 YCDKDKQSHPSIQLKKEKMKLAQKESARPRITFRAGVGSNNMESAAHPWFICTS 180
DB 121 YCDKDKQSHPSIQLKKEKMKLAQKESARPRITFRAGVGSNNMESAAHPWFICTS 180
QY 181 CNCNEPVGVTDKFENRKHIEFSFOVCKAEMSPSEVSD 218
DB 181 CNCNEPVGVTDKFENRKHIEFSFOVCKAEMSPSEVSD 218
RESULT 3
US-09-965-528-25
Sequence 25, Application US/09965528
Publication No. US20020187523A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BURFORD, Neil
APPLICANT: BANDMAN, Olga
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dzung Anna M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0701 USA
CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949

PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: 60/146,700
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/157,508
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020187523A1 4365383CD1
US-09-965-528-25

Query Match 29.8%; Score 65; DB 9; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.3e-53; Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MNFVTSRKVKSINPKKFSIHDDHKVLVDSGNLIAVPDKNYIRPEIFPALASSLSAS 102
DB 1 MNFVTSRKVKSINPKKFSIHDDHKVLVDSGNLIAVPDKNYIRPEIFPALASSLSAS 60
QY 103 AEKGS 107
DB 61 AEKGS 65

RESULT 4
US-09-969-984-25
Sequence 25, Application US/09969984
Publication No. US20040048244A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BURFORD, Neil
APPLICANT: BANDMAN, Olga
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dzung Anna M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0701-1 USA
CURRENT APPLICATION NUMBER: US/09/969,984
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/134,949; 60/144,270; 60/146,700; 60/157,508
PRIOR FILING DATE: 1999-05-19; 1999-07-15; 1999-07-30; 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040048244A1 4365383CD1
US-09-969-984-25

Query Match 29.8%; Score 65; DB 11; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.3e-53; Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MNFVTSRKVKSINPKKFSIHDDHKVLVDSGNLIAVPDKNYIRPEIFPALASSLSAS 102
DB 1 MNFVTSRKVKSINPKKFSIHDDHKVLVDSGNLIAVPDKNYIRPEIFPALASSLSAS 60
QY 103 AEKGS 107
DB 61 AEKGS 65

Db 61 AEXGS 65

RESULT 5

US-10-095-407-5

Sequence 5, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 115

TYPE: PR

ORGANISM: Homo sapiens

US-10-095-407-5

Query Match 25.2%; Score 55; DB 13; Length 115;

Best Local Similarity 100.0%; Pred. No. 3.2e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 163

6 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 60

RESULT 6

US-10-095-407-9

Sequence 9, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 9

LENGTH: 115

TYPE: PR

ORGANISM: Homo sapiens

US-10-095-407-9

Query Match 25.2%; Score 55; DB 13; Length 115;

Best Local Similarity 100.0%; Pred. No. 3.2e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 163

6 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 60

RESULT 7

US-10-095-407-13

Sequence 13, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 115

TYPE: PR

ORGANISM: Homo sapiens

US-10-095-407-13

Query Match 25.2%; Score 55; DB 13; Length 115;

Best Local Similarity 100.0%; Pred. No. 3.2e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 163

6 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 60

RESULT 8

US-10-095-407-11

Sequence 11, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 11

LENGTH: 136

TYPE: PR

ORGANISM: Homo sapiens

US-10-095-407-11

Query Match 25.2%; Score 55; DB 13; Length 136;

Best Local Similarity 100.0%; Pred. No. 3.7e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 163

27 ILGVSKGEFCLYCDKDKGSHPSLQKKKMLKLAQKESARRPFIYRAQVGS 81

RESULT 9

US-09-876-790-10

Sequence 10, Application US/09876790

Publication No. US20030091532A1

GENERAL INFORMATION:

APPLICANT: SIMS, John E.

APPLICANT: SMITH, Dirk E.

APPLICANT: BORN, Teresa L.

TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTID

FILE REFERENCE: 2008-US

CURRENT APPLICATION NUMBER: US/09/876,790

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 60/112,163

PRIOR FILING DATE: 1998-12-14

PRIOR APPLICATION NUMBER: 60/146,675

PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-10

Query Match 25.2%; Score 55; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 163
Db 48 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 102

RESULT 10
US-10-302-554-9
Sequence 9, Application US/10302554
Publication No. US20030148467A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Shepard, Paul O.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
FILE REFERENCE: 98-59
CURRENT APPLICATION NUMBER: US/10/302,554
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/428,118
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 60/105,824
PRIOR FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-302-554-9

Query Match 25.2%; Score 55; DB 14; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 163
Db 48 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 102

RESULT 11
US-10-302-554-15
Sequence 15, Application US/10302554
Publication No. US20030148467A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Shepard, Paul O.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
FILE REFERENCE: 98-59
CURRENT APPLICATION NUMBER: US/10/302,554
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/428,118
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 60/105,824
PRIOR FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 157

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant protein
US-10-302-554-15

Query Match 25.2%; Score 55; DB 14; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 163
Db 48 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 102

RESULT 12
US-10-888-918-10
Sequence 10, Application US/10888918
Publication No. US20040248187A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/10/888,918
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/876,790
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-888-918-10

Query Match 25.2%; Score 55; DB 16; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 163
Db 48 ILGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQVGS 102

RESULT 13
US-10-888-867-10
Sequence 10, Application US/10888867
Publication No. US2005009075A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/10/888,867
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/876,790
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-888-867-10

Query Match 25.2%; Score 55; DB 17; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 14
US-10-888-779-10
Sequence 10, Application US/10888779
Publication No. US2005009138A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/10/888, 779
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/876, 790
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-888-779-10

Query Match 25.2%; Score 55; DB 17; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 15
US-10-888-780-10
Sequence 10, Application US/10888780
Publication No. US20050013797A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/10/888, 780
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/876, 790
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-888-780-10

Query Match 25.2%; Score 55; DB 17; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 16
US-10-888-931-10
Sequence 10, Application US/10888931
Publication No. US20050013798A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/10/888, 931
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/876, 790
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-888-931-10

Query Match 25.2%; Score 55; DB 17; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 17
US-10-095-407-7
Sequence 7, Application US/10095407
Publication No. US20020164330A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 167

TYPE: PRT
ORGANISM: Homo sapiens
US-10-095-407-7

Query Match 25.2%; Score 55; DB 13; Length 167;
Best Local Similarity 100.0%; Pred. No. 4,4e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163
Db 58 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 112

RESULT 18
US-10-095-407-2
Sequence 2, Application US/10095407
Publication No. US20020164330A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-10-095-407-2

Query Match 25.2%; Score 55; DB 13; Length 178;
Best Local Similarity 100.0%; Pred. No. 4,6e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163
Db 69 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 123

RESULT 19
US-10-139-833-11
Sequence 11, Application US/10139833
Publication No. US20030004106A1
GENERAL INFORMATION:
APPLICANT: Sarris, Christiaan M.
APPLICANT: Giles, Jennifer
APPLICANT: Mu, Sharon X.
APPLICANT: Xia, Min
APPLICANT: Baes, Michael B.
APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 60/195,910
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-833-11

Query Match 25.2%; Score 55; DB 14; Length 178;
Best Local Similarity 100.0%; Pred. No. 4,6e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163
Db 69 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 123

RESULT 20
US-09-876-790-3
Sequence 3, Application US/09876790
Publication No. US20030091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XREC2 DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-3

Query Match 25.2%; Score 55; DB 10; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163
Db 83 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 137

RESULT 21
US-10-139-833-13
Sequence 13, Application US/10139833
Publication No. US20030004106A1
GENERAL INFORMATION:
APPLICANT: Sarris, Christiaan M.
APPLICANT: Giles, Jennifer
APPLICANT: Mu, Sharon X.
APPLICANT: Xia, Min
APPLICANT: Baes, Michael B.
APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 60/195,910

;; PRIOR FILING DATE: 2000-04-10
;; PRIOR APPLICATION NUMBER: 09/724,583
;; PRIOR FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-139-833-13

Query Match 25.2%; Score 55; DB 14; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

RESULT 22

US-10-888-918-3
;; Sequence 3, Application US/10888918
;; Publication No. US20040248187A1
;; GENERAL INFORMATION:
;; APPLICANT: SIMS, John E.
;; APPLICANT: SMITH, Dirk E.
;; APPLICANT: BORN, Teresa L.
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE2 DNAS AND POLYPEPTI
;; FILE REFERENCE: 2008-US
;; CURRENT APPLICATION NUMBER: US/10/888,918
;; CURRENT FILING DATE: 2004-07-09
;; PRIOR APPLICATION NUMBER: US/09/876,790
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/112,163
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: 60/146,675
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR FILING DATE: 1999-12-14
;; PRIOR APPLICATION NUMBER: PCT/US99/29549
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-888-918-3

Query Match 25.2%; Score 55; DB 16; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

RESULT 23

US-10-888-867-3
;; Sequence 3, Application US/10888867
;; Publication No. US2005009075A1
;; GENERAL INFORMATION:
;; APPLICANT: SIMS, John E.
;; APPLICANT: SMITH, Dirk E.
;; APPLICANT: BORN, Teresa L.
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE2 DNAS AND POLYPEPTI
;; FILE REFERENCE: 2008-US
;; CURRENT APPLICATION NUMBER: US/10/888,867
;; CURRENT FILING DATE: 2004-07-09
;; PRIOR APPLICATION NUMBER: US/09/876,790
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/112,163
;; PRIOR FILING DATE: 1998-12-14

;; PRIOR APPLICATION NUMBER: 60/146,675
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: PCT/US99/29549
;; PRIOR FILING DATE: 1999-12-14
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-888-867-3

Query Match 25.2%; Score 55; DB 17; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

RESULT 24

US-10-888-779-3
;; Sequence 3, Application US/10888779
;; Publication No. US2005009138A1
;; GENERAL INFORMATION:
;; APPLICANT: SIMS, John E.
;; APPLICANT: SMITH, Dirk E.
;; APPLICANT: BORN, Teresa L.
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE2 DNAS AND POLYPEPTI
;; FILE REFERENCE: 2008-US
;; CURRENT APPLICATION NUMBER: US/10/888,779
;; CURRENT FILING DATE: 2004-07-09
;; PRIOR APPLICATION NUMBER: US/09/876,790
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/112,163
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: 60/146,675
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR FILING DATE: 1999-12-14
;; PRIOR APPLICATION NUMBER: PCT/US99/29549
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-888-779-3

Query Match 25.2%; Score 55; DB 17; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

RESULT 25

US-10-888-780-3
;; Sequence 3, Application US/10888780
;; Publication No. US20050013797A1
;; GENERAL INFORMATION:
;; APPLICANT: SIMS, John E.
;; APPLICANT: SMITH, Dirk E.
;; APPLICANT: BORN, Teresa L.
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE2 DNAS AND POLYPEPTI
;; FILE REFERENCE: 2008-US
;; CURRENT APPLICATION NUMBER: US/10/888,780
;; CURRENT FILING DATE: 2004-07-09
;; PRIOR APPLICATION NUMBER: US/09/876,790
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/112,163

```

; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-780-3

Query Match
Best Local Similarity 100.0%; Score 55; DB 17; Length 192;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVGS 163
Db 83 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVGS 137

RESULT 26
US-10-888-931-3
; Sequence 3, Application US/10888931
; Publication No. US20050013798A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECB DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,931
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-931-3

Query Match
Best Local Similarity 100.0%; Score 55; DB 17; Length 192;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVGS 163
Db 83 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVGS 137

RESULT 27
US-10-006-867-142
; Sequence 142, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090688
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091628
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/096012
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096757
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096949
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/096959
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/097954
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097971
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097979
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
```

PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105881
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/106030
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106856
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108807
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/112419
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112853
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113011
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/112854
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113408
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114223
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/115614

PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116527
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/119285
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119287
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119525
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/120014
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/129122
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/129674
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/199397
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

Query Match 25.2%; Score 55; DB 13; Length 193;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGPERCLYCDXKQSHPSLQKKKLMKLAQKESARRPIFYRAQVGS 163
DB 84 ILGVSKGPERCLYCDXKQSHPSLQKKKLMKLAQKESARRPIFYRAQVGS 138

RESULT 28
US-10-063-547-142
Sequence 142, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 142
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-547-142

Query Match 25.2%; Score 55; DB 13; Length 193;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163
DB 84 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 138

RESULT 29

US-10-063-551-142
; Sequence 142, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:

; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 142
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-142

Query Match 25.2%; Score 55; DB 13; Length 193;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163
DB 84 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 138

RESULT 30

US-10-063-616-142
; Sequence 142, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:

; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 142

; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-616-142

Query Match 25.2%; Score 55; DB 14; Length 193;
Best Local Similarity 100.0%; Pred. No. 5e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163
DB 84 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 138

Search completed: October 3, 2005, 11:50:26
Job time : 166 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 11:42:18 ; Search time 16 Seconds
(without alignments)
1310.953 Million cell updates/sec

Title: US-10-694-978-2
Perfect score: 218
Sequence: 1 MSFVGENSGVKGSEDEKED.....IEFSPQVCKAEMSPSEVSD 218

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.7	413	2 H72606	hypothetical prote
2	8	3.7	982	2 T06576	probable protein K
3	8	3.7	993	2 T17230	hypothetical prote
4	8	3.7	1427	2 T39219	acp-binding caset
5	8	3.7	1622	2 D86428	glutathione S-conj
6	8	3.7	2118	2 T13612	hypothetical prote
7	7	3.2	116	2 E72509	probable non speci
8	7	3.2	117	2 G87095	conserved membrane
9	7	3.2	118	1 DNMTU3	NADH2 dehydrogenas
10	7	3.2	118	1 DNMTU3	NADH2 dehydrogenas
11	7	3.2	118	2 S71077	NADH2 dehydrogenas
12	7	3.2	118	2 S71079	NADH2 dehydrogenas
13	7	3.2	118	2 T09501	probable NADH2 den
14	7	3.2	118	2 S70000	NADH2 dehydrogenas
15	7	3.2	130	2 B72531	NADH2 dehydrogenas
16	7	3.2	132	2 F96779	probable ribosomal
17	7	3.2	133	2 F71189	hypothetical prote
18	7	3.2	138	2 G97191	probable membrane
19	7	3.2	178	2 JB0264	cyelin 1 - human
20	7	3.2	179	2 AD2007	hypothetical prote
21	7	3.2	185	2 T49611	hypothetical prote
22	7	3.2	208	2 T52450	ribosomal protein
23	7	3.2	209	2 A75032	hypothetical prote
24	7	3.2	220	2 E72210	hypothetical prote
25	7	3.2	221	2 A72097	probable ABC trans
26	7	3.2	221	2 G86525	probable ABC trans
27	7	3.2	251	2 AC2187	phospho-2-dehydro
28	7	3.2	265	2 T42957	hypothetical prote
29	7	3.2	290	2 H90001	lipoprotein precur

30	7	3.2	301	2 T18788	hypothetical prote
31	7	3.2	303	2 E81348	binding-protein de
32	7	3.2	305	2 G70382	phosphoridylglycer
33	7	3.2	307	2 F69898	hypothetical prote
34	7	3.2	352	2 T51234	scarcecrow-like pro
35	7	3.2	356	2 C70025	multitiding-efflux t
36	7	3.2	366	2 T26038	hypothetical prote
37	7	3.2	367	2 C90399	iron-containing al
38	7	3.2	382	2 F82428	hypothetical prote
39	7	3.2	421	2 T02135	transcription enha
40	7	3.2	506	2 A40679	transcription enha
41	7	3.2	523	2 B40679	transcription enha
42	7	3.2	523	2 A86287	hypothetical prote
43	7	3.2	593	2 E86347	scarcecrow-like 1 p
44	7	3.2	603	2 B96578	hypothetical prote
45	7	3.2	614	2 AB3596	periplasmic oligop
46	7	3.2	770	2 A12421	hypothetical prote
47	7	3.2	863	2 B64138	uridylyltransferas
48	7	3.2	946	2 S48255	probable membrane
49	7	3.2	964	2 T30455	hypothetical prote
50	7	3.2	1014	2 H86438	protein T19E23.7 [
51	7	3.2	1257	2 S28764	neurocan precursor
52	7	3.2	1268	2 S52781	neurocan - mouse
53	7	3.2	1609	2 S25345	probable membrane
54	7	3.2	2515	2 S47008	tenascin-like prot
55	7	3.2	2559	2 T09144	probable guanine n
56	7	3.2	2870	2 H96974	cyclic beta 1-2 gl
57	7	3.2	4056	2 H96599	protein F14f16.10
58	7	2.8	14	2 PH0774	t-cell receptor be
59	6	2.8	31	2 S49191	hypothetical prote
60	6	2.8	38	2 S32314	sinapine synthase
61	6	2.8	47	2 T29970	hypothetical prote
62	6	2.8	50	2 H82804	hypothetical prote
63	6	2.8	54	2 T07247	hypothetical prote
64	6	2.8	56	2 C83988	hypothetical prote
65	6	2.8	61	2 H83614	hypothetical prote
66	6	2.8	66	2 T15539	hypothetical prote
67	6	2.8	69	1 B56085	copper homeostasis
68	6	2.8	71	2 D81389	hypothetical prote
69	6	2.8	73	2 T77305	hemoglobin beta-1
70	6	2.8	73	2 T77306	hemoglobin beta-3
71	6	2.8	83	2 J01962	hypothetical 9.3K
72	6	2.8	85	2 S68315	ferritin H chain -
73	6	2.8	89	2 T69150	perc protein - Esc
74	6	2.8	91	2 J80036	Clara cell 10K pro
75	6	2.8	94	2 B84281	hypothetical prote
76	6	2.8	96	2 AG1502	probable cell surf
77	6	2.8	98	2 H84744	hypothetical prote
78	6	2.8	99	2 D81074	hypothetical prote
79	6	2.8	100	2 D71164	hypothetical prote
80	6	2.8	101	2 D70710	hypothetical prote
81	6	2.8	102	2 T53094	gene Pax-1 protein
82	6	2.8	103	2 G72577	hypothetical prote
83	6	2.8	104	2 S17125	phage shock protei
84	6	2.8	105	2 T46584	hypothetical prote
85	6	2.8	107	2 S07818	homeotic protein H
86	6	2.8	108	2 T50348	ribosomal protein
87	6	2.8	111	2 D81780	probable integral
88	6	2.8	114	2 A81204	multitiding resista
89	6	2.8	114	2 S48982	hypothetical prote
90	6	2.8	117	2 E42519	A2i1.13.6K protein
91	6	2.8	117	2 D36850	A20L protein - var
92	6	2.8	117	2 T28562	hypothetical prote
93	6	2.8	117	2 B72166	hypothetical prote
94	6	2.8	118	2 S71081	A2iL protein - var
95	6	2.8	118	2 B90259	NADH2 dehydrogenas
96	6	2.8	120	2 T16510	hypothetical prote
97	6	2.8	128	2 C69195	hypothetical prote
98	6	2.8	133	2 H90989	hypothetical prote
99	6	2.8	133	2 C85835	hypothetical prote
100	6	2.8	125	2 AC0753	flagellar protein
101	6	2.8	125	2 S78697	probable export pr
102	6	2.8	127	2 C85091	arabinogalactan-pr

103	6	2.8	130	2	G72609	hypothetical prote
104	6	2.8	132	1	RS5814	ribosomal protein
105	6	2.8	132	1	T43826	ribosomal protein
106	6	2.8	132	2	F84322	50S ribosomal prot
107	6	2.8	132	2	I52524	testis lipid bindi
108	6	2.8	133	1	A47416	ubiquitin-like pro
109	6	2.8	133	2	A34248	ribosomal protein
110	6	2.8	133	2	PC4011	fatty acid-binding
111	6	2.8	133	2	T24099	hypothetical prote
112	6	2.8	133	2	P97840	hypothetical prote
113	6	2.8	133	2	I48346	ribosomal protein
114	6	2.8	134	2	D64558	hypothetical prote
115	6	2.8	134	2	F71949	hypothetical prote
116	6	2.8	136	2	T26814	hypothetical prote
117	6	2.8	137	2	E64845	ycdv protein - Esc
118	6	2.8	139	2	A83140	hypothetical prote
119	6	2.8	140	2	C71176	hypothetical prote
120	6	2.8	141	2	I48109	ferritin heavy cha
121	6	2.8	141	2	T17849	hypothetical prote
122	6	2.8	141	2	AC1994	hypothetical prote
123	6	2.8	141	2	A86417	probable auxin-ind
124	6	2.8	142	2	T30401	hypothetical prote
125	6	2.8	143	1	H69283	conserved hypotet
126	6	2.8	143	2	S04588	hemoglobin beta ch
127	6	2.8	144	2	S71764	narbonin (clone pN
128	6	2.8	145	2	S76877	hypothetical prote
129	6	2.8	146	1	HB8TF	hemoglobin beta ch
130	6	2.8	146	1	HBEMA	hemoglobin beta ch
131	6	2.8	146	1	HBFXB	hemoglobin beta ch
132	6	2.8	146	1	HBGP	hemoglobin beta ch
133	6	2.8	146	1	HBHY	hemoglobin beta ch
134	6	2.8	146	1	HBMSN1	hemoglobin beta ml
135	6	2.8	146	1	HBOSE	hemoglobin beta ch
136	6	2.8	146	1	HBTSM	hemoglobin beta ch
137	6	2.8	146	1	HBVOY	hemoglobin beta ch
138	6	2.8	146	1	HGBAY	hemoglobin gamma c
139	6	2.8	146	1	HGMQJ	hemoglobin gamma c
140	6	2.8	146	1	HGMQP	hemoglobin gamma c
141	6	2.8	146	2	A34947	hemoglobin beta ch
142	6	2.8	146	2	B29392	hemoglobin beta ch
143	6	2.8	146	2	B29391	hemoglobin beta ch
144	6	2.8	146	2	B25729	hemoglobin beta ch
145	6	2.8	146	2	B25359	hemoglobin beta ch
146	6	2.8	146	2	B24690	hemoglobin beta-S
147	6	2.8	146	2	JU0163	hemoglobin beta ch
148	6	2.8	147	1	S13398	PTS fructose-speci
149	6	2.8	147	1	I37025	hemoglobin gamma-G
150	6	2.8	147	1	HBMS	hemoglobin beta ma

ALIGNMENTS

RESULT 1
H72606
hypothetical protein APE1319 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: H72606
R/Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: H72606
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-413 <KAW>
A/Cross-references: UNIPROT:Q9YCD8; DDBJ:AP000061; NID:95104821; PIDN:BA080310.1; PID:cl
A/Experimental source: strain K1
C/Genetics:
A/Gene: APE1319

Query Match 3.7%; Score 8; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 LASSLSA 101
Db 12 LASSLSA 19

RESULT 2

T06576
probable protein kinase TCTR2 - tomato
C/Species: Lycopersicon esculentum (tomato)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06576
R/Hackett, R. M.
submitted to the EMBL Data Library, March 1998
A/Reference number: Z15770
A/Accession: T06576
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-982 <HAC>
A/Cross-references: UNIPROT:O55833; EMBL:AJ005077; NID:e1296722; PIDN:CA06334.1; PID:el
A/Experimental source: cultivar Ailsa Craig
C/Genetics:
A/Gene: TCTR2

Query Match 3.7%; Score 8; DB 2; Length 982;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 ASSLSAS 102
Db 30 ASSLSAS 37

RESULT 3

T17230
hypothetical protein DKFZp434E066.1 - human
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T17230
R/Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A/Reference number: Z18722
A/Accession: T17230
A/Status: preliminary
A/Molecule type: RNA
A/Residues: 1-993 <ROE>
A/Cross-references: UNIPROT:Q9UES6; EMBL:AL117432
A/Experimental source: adult testis; clone DKFZp434E066
C/Genetics:
A/Note: DKFZp434E066.1

Query Match 3.7%; Score 8; DB 2; Length 993;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSSS 100
Db 7 ALASSSS 14

RESULT 4

T39219
atp-binding cassette transporter abcl - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T39219
R/McDougal, R.; Barrett, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A/Reference number: Z21836
A/Accession: T39219

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1427 <MCD>
A;Cross-references: UNIPROT:Q93337; EMBL:Z99262; PDB:CA16410.1; GSPDB:GN00066; SPDB:SF
A;Experimental source: strain 972h; contid c9E9
C;Genetics:
A;Gene: SPDB:SPAC9E9.12c
A;Map position: 1
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1427;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLDSC 75
Db 1391 KVLVLDSC 1398

RESULT 5
D86428
glutathione S-conjugate transporting ATPase (AtMRP1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86428
R;Theologian, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86428
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1622 <STO>
A;Cross-references: UNIPROT:Q9C8G9; GB:A8005172; NID:g11055814; PDB:AA628284.1; GSPDB:C
C;Genetics:
A;Map position: 1
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1622;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLDSC 75
Db 1440 KVLVLDSC 1447

RESULT 6
T13612
hypothetical protein 8D8.1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13612
R;Papadimitrakaki, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17695
A;Accession: T13612
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2118 <PAP>
A;Cross-references: UNIPROT:O76904; EMBL:AL022018; PDB:CA17682.1
C;Genetics:
A;Cross-references: FlyBase:FBgn0024367
A;Intons: 47/3; 726/3; 770/1; 813/3; 1404/1; 1473/3
A;Note: EG:8D8.1

C;Superfamily: Drosophila hypothetical protein EG_8D8.1

Query Match 3.7%; Score 8; DB 2; Length 2118;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SSLSASA 103
Db 76 SSLSASA 83

RESULT 7
E72509
probable non specific lipid-transfer protein APE2051 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72509
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ka
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:9310339; PMID:10382966
A;Accession: E72509
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-116 <XAM>
A;Cross-references: UNIPROT:Q9YA88; DDBJ:AP000063; NID:g5105654; PDB:BA81061.1; PID:dlc
A;Experimental source: strain KI
C;Genetics:
A;Gene: APE2051

Query Match 3.2%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SSLSASA 102
Db 39 SSLSASA 45

RESULT 8
G87095
conserved membrane protein ML1494 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87095
R;Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
R.; Davies, R.M.; Devlin, K.; Dutfoy, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sqr
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: G87095
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <STO>
A;Cross-references: UNIPROT:Q9CBK5; GB:AL450380; NID:g13093338; PDB:CAK30444.1; GSPDB:GT
C;Genetics:
A;Gene: ML1494
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1171

Query Match 3.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 LILLGVS 114
Db 98 LILLGVS 104

RESULT 9
DNMTU3

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - wheat mitochondrion
C/Species: mitochondrion Triticum aestivum (common wheat)
C/Date: 30-Jun-1992 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C/Accession: JQ1374; S03609
R/Guadaberto, J.M.; Bonnard, G.; Lamattina, L.; Grienenberger, J.M.
Plant Cell 3, 1109-1120, 1991
A/Title: Expression of the wheat mitochondrial nad3-rps12 transcription unit: correlatio
A/Reference number: JQ1374; MUID:92338836; PMID:1726558
A/Accession: JQ1374
A/Molecule type: mRNA
A/Residues: 1-118 <GUA>
A/Cross-references: UNIPROT:P60160; GB:X59153; GB:S40874; NID:g433681
A/Note: In plant mitochondria, RNA editing involves the conversion of C in the primary
R/Note: this sequence is the translation of the consensus sequence of three cDNA clones
R/Guadaberto, J.M.; Wintz, H.; Weil, J.H.; Grienenberger, J.M.
Mol. Gen. Genet. 215, 116-127, 1988
A/Title: The genes coding for subunit 3 of NADH dehydrogenase and for ribosomal protein
A/Reference number: S03609; MUID:89201232; PMID:2853827
A/Accession: S03609
A/Molecule type: DNA
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-45,'S',47-48,'S',50-63,'P',65-69,'P',7
A/Cross-references: EMBL:X14262; NID:g13703; PIDN:CAA32475.1; PID:g13704
C/Genetics:
A/Gene: nad3
A/Genome: mitochondrion
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.2%; Score 7; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 STILLGV 113
DB 18 STILLGV 24
RESULT 10
DNZM2
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - maize mitochondrion
C/Species: mitochondrion Zea mays (maize)
C/Date: 30-Jun-1992 #sequence_revision 28-Aug-1998 #text_change 09-Jul-2004
C/Accession: S70025; S70024; S05952
R/Groskopf, D.; Mulligan, R.M.
Curr. Genet. 29, 556-563, 1996
A/Title: Developmental- and tissue-specificity of RNA editing in mitochondria of suspens
A/Reference number: S70024; MUID:96269915; PMID:8662195
A/Accession: S70025
A/Molecule type: mRNA
A/Residues: 1-118 <GRO>
A/Cross-references: UNIPROT:P16265
A/Experimental source: Cultivar Black Mexican Sweet
A/Note: In plant mitochondria, RNA editing involves the conversion of C in the primary
A/Accession: S70024
A/Molecule type: DNA
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-45,'L',47-48,'S',50-61,'P',63,'P',65-6
R/Guadaberto, J.M.; Wintz, H.; Weil, J.H.; Grienenberger, J.M.
Mol. Gen. Genet. 215, 118-127, 1988
A/Title: The genes coding for subunit 3 of NADH dehydrogenase and for ribosomal protein
A/Reference number: S03609; MUID:89201232; PMID:2853827
A/Accession: S05952
A/Molecule type: DNA
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-45,'S',47-48,'S',50-61,'P',63,'P',65-6
A/Cross-references: EMBL:X14709; NID:g13913; PIDN:CAA32833.1; PID:g13914
A/Experimental source: strain WF9-N
A/Note: the authors translated the codon CCG for residue 62 as Leu
C/Genetics:
A/Gene: nad3
A/Genome: mitochondrion
C/Function:
A/Pathway: respiratory chain
A/Note: FAD cofactor

C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.2%; Score 7; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 STILLGV 113
DB 18 STILLGV 24
RESULT 11
S71077
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - common sunflower mitochondrion
C/Species: mitochondrion Helianthus annuus (common sunflower)
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S71077; S71076
R/Perrotta, G.; Regina, T.M.R.; Ceci, L.R.; Quagliariello, C.
Mol. Gen. Genet. 251, 326-337, 1996
A/Title: Conservation of the organization of the mitochondrial nad3 and rps12 genes in e
A/Reference number: S71076; MUID:96262185; PMID:8676875
A/Accession: S71077
A/Molecule type: mRNA
A/Residues: 1-118 <PER>
A/Cross-references: UNIPROT:P60159; EMBL:Z49775; NID:g1518349; PIDN:CAA89856.1; PID:g151
A/Note: 2-Leu, 15-Leu, 21-Leu, 27-Leu, 70-Phe, 72-Leu, 77-Phe, 83-Ser, 89-Leu, 92-Phe, 10
A/Accession: S71076
A/Molecule type: DNA
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-69,'P',71,'P',73-76,'S',78-82,'P',84-86
A/Cross-references: EMBL:Z49774; NID:g1518346; PIDN:CAA89854.1; PID:g1518347
C/Genetics:
A/Gene: nad3
A/Genome: mitochondrion
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.2%; Score 7; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 STILLGV 113
DB 18 STILLGV 24
RESULT 12
S71079
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Magnolia soulangeana mitochondrion
C/Species: mitochondrion Magnolia soulangeana
C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C/Accession: S71079; S71078
R/Perrotta, G.; Regina, T.M.R.; Ceci, L.R.; Quagliariello, C.
Mol. Gen. Genet. 251, 326-337, 1996
A/Title: Conservation of the organization of the mitochondrial nad3 and rps12 genes in e
A/Reference number: S71076; MUID:96262185; PMID:8676875
A/Accession: S71079
A/Molecule type: mRNA
A/Residues: 1-118 <PER>
A/Cross-references: UNIPROT:Q96037; EMBL:Z49796; NID:g1518358; PIDN:CAA89888.1; PID:g151
A/Note: 2-Leu, 5-Val, 15-Leu, 21-Leu, 27-Leu, 42-Tyr, 46-Phe, 49-Phe, 62-Leu, 70-Phe, 72-
A/Accession: S71078
A/Molecule type: DNA
A/Residues: 1,'S',3-4,'A',6-14,'P',16-20,'P',22-26,'P',28-41,'H',43-45,'S',47-48,'S',50-6
A/Cross-references: EMBL:Z49797; NID:g1518355; PIDN:CAA89890.1; PID:g1518356
C/Genetics:
A/Gene: nad3
A/Genome: mitochondrion
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.2%; Score 7; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;

Query Match	3.2%;	Score 7;	DB 2;	Length 118;
Best Local Similarity	100.0%;	Pred. No. 20;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;
QY	107	SLIRLGV	113	
Db	18	SLIRLGV	24	

RESULT 17
F71189
hypochemical protein PH1790 - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #ext_change 09-Jul-2004
C:Accession: F71189
C:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A/Reference number: A71000; PMID:98344137; PMID:9679194
 A/Accession: F71189
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-133 <RAW>
 A/Cross-references: UNIPROT:Q59454; GB:AP000007; NID:G3236134; PIDN:BAA30909.1; PID:G325
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C/Genetics:
 A/Gene: PH1790

Query Match 3.2%; Score 7; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 SLSSAS 102
 |||||
 Db 68 SLSSAS 74

RESULT 18
 G97191

probable membrane protein [imported] - Clostridium acetobutylicum
 C/Species: Clostridium acetobutylicum
 C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C/Accession: G97191
 R/Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A/Reference number: A96500; PMID:21359325; PMID:21359325
 A/Accession: G97191
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-138 <KUR>
 A/Cross-references: UNIPROT:Q97GK0; GB:AE001437; PIDN:AAK80322.1; PID:G15025378; GSPDB:G
 A/Experimental source: Clostridium acetobutylicum ATCC6824
 C/Genetics:
 A/Gene: CAC2366

Query Match 3.2%; Score 7; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 GSLLLG 112
 |||||
 Db 30 GSLLLG 36

RESULT 19
 JE0264
 cyclin I - human
 C/Species: Homo sapiens (man)
 C/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
 C/Accession: JE0264
 R/Zhu, X.; Naz, R.K.
 Biochem. Biophys. Res. Commun. 249, 56-60, 1998
 A>Title: Expression of a novel isoform of cyclin I in human testis.
 A/Reference number: JE0264; PMID:98381026; PMID:9705831
 A/Accession: JE0264
 A/Molecule type: mRNA
 A/Residues: 1-178 <ZHU>
 A/Cross-references: UNIPROT:Q14094
 C/Comment: This protein may have a physiological role in spermatogenesis and/or human sp

Query Match 3.2%; Score 7; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 PALASSL 98

Db |||||
 66 PALASSL 72

RESULT 20
 AD2007
 hypothetical protein all1610 [imported] - Nostoc sp. (strain PCC 7120)
 C/Species: Nostoc sp. PCC 7120
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C/Accession: AD2007
 R/Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat
 A/Reference number: AB1807; PMID:21595285; PMID:11759840
 A/Accession: AD2007
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-179 <KUR>
 A/Cross-references: UNIPROT:Q9YMK3; GB:BA000019; PIDN:BAW77976.1; PID:G17135430; GSPDB:G
 A/Experimental source: strain PCC 7120
 C/Genetics:
 A/Gene: all1610

Query Match 3.2%; Score 7; DB 2; Length 179;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 SLILGV 113
 |||||
 Db 121 SLILGV 127

RESULT 21
 T49611
 hypothetical protein B3E4.240 [imported] - Neurospora crassa
 C/Species: Neurospora crassa
 C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C/Accession: T49611
 R/Schulte, U.; Aign, V.; Hohnel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
 A/Reference number: Z25022
 A/Accession: T49611
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-165 <SCH>
 A/Cross-references: UNIPROT:Q9PSV8; EMBL:AL355931; GSPDB:GN00116; NCSP:B3E4.240
 A/Experimental source: BAC clone B3E4; strain OR74A
 C/Genetics:
 A/Gene: NCSP:B3E4.240
 A/Map position: 6

Query Match 3.2%; Score 7; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SLSSASA 103
 |||||
 Db 34 SLSSASA 40

RESULT 22
 T52450
 ribosomal protein S9 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
 C/Accession: T52450
 R/Arimura, S.; Takusagawa, S.; Hatano, S.; Nakazono, M.; Hirai, A.; Tsutsumi, N.
 FEBS Lett. 450, 231-234, 1999
 A>Title: A novel plant nuclear gene encoding chloroplast ribosomal protein S9 has a trans
 A/Reference number: Z26079
 A/Accession: T52450

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-208 <ARN>
A:Cross-references: UNIPROT:Q9XJ27; EMBL:AB022676; PIDD:BA02396.1
C:Gene: rps9
A:Gene: rps9
C:Superfamily: ribosomal protein S9/S16

Query Match 3.2%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 94 LASLSS 100
DB 7 LASLSS 13

RESULT 23
A75032
hypothetical protein PAB1558 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A75032
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: A75032
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209 <RNA>
A:Cross-references: UNIPROT:Q9UZA9; GB:AJ248287; GB:AL096836; NID:G5458657; PIDD:CA5015
A:Experimental source: strain Orsay
C:Gene: PAB1558

Query Match 3.2%; Score 7; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 52 VKSLNP 58
DB 193 VKSLNP 199

RESULT 24
E72210
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: E72210
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence
A:Reference number: A72200; M0ID:99287316; PMID:10360571
A:Accession: E72210
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <ARN>
A:Cross-references: UNIPROT:Q9X2C0; GB:AE001817; GB:AE000512; NID:G4982370; PIDD:ADJ3686
A:Experimental source: strain MSB8
C:Gene: TMI800

Query Match 3.2%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 164 RNMLESA 170
DB 185 RNMLESA 191

RESULT 25
A72097
probable ABC transporter permease protein - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: A72097
R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; M0ID:99206606; PMID:10192388
A:Accession: A72097
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <ARN>
A:Cross-references: UNIPROT:Q9Z8Q9; GB:AE001613; GB:AE001363; NID:G4376550; PIDD:ADJ1842
A:Experimental source: strain CWL029
C:Gene: CP0279
C:Superfamily: ABC transporter permease protein

Query Match 3.2%; Score 7; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 53 KSINPK 59
DB 44 KSINPK 50

RESULT 26
G86525
Probable ABC transporter permease protein [imported] - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86525
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Iet Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: A86491; M0ID:20330349; PMID:10871362
A:Accession: G86525
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <STO>
A:Cross-references: UNIPROT:Q9Z8Q9; GB:BA000008; NID:G8978653; PIDD:BA98489.1; GSPDB:GNC
A:Experimental source: strain J138
C:Gene: CP10279
C:Superfamily: ABC transporter permease protein

Query Match 3.2%; Score 7; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 53 KSINPK 59
DB 44 KSINPK 50

RESULT 27
AC2187
Phospho-2-dehydro-3-deoxyphosphate aldolase/chorismate mutase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004
C:Accession: AC2187
R:Keneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; M0ID:21595285; PMID:11759840
A:Accession: AC2187

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <KUR>
A:Cross-references: UNIPROT:Q8YSN4; GB:BA000019; PIDN:BA074749.1; PID:G17132144; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: a1r3050
C:Superfamily: 2-dehydro-3-deoxyphosphoocetate aldolase

Query Match 3.2%; Score 7; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 QVGSRRM 166
DB 79 QVGSRRM 85

RESULT 28

T42957
hypothetical protein 42 - ateline herpesvirus 3 (strain 73)

C:Species: ateline herpesvirus 3

A:Variety: strain 73

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42957

R:Albrecht, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, August 1998

A:Description: Primary structure of the herpesvirus ateles genome.

A:Reference number: Z22274

A:Accession: T42957

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-265 <ALB>

A:Cross-references: UNIPROT:Q9YTM3; EMBL:AF083424; PIDN:AAC95568.1

A:Experimental source: strain 73

C:Superfamily: hypothetical protein ORF42

Query Match 3.2%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILLGVSK 115
DB 7 ILLGVSK 13

RESULT 29

H90001
lipoprotein precursor [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H90001

R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H90001

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-290 <KUR>

A:Cross-references: UNIPROT:Q99SG7; GB:BA000018; PID:G13701885; PIDN:BA043177.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA1893

C:Superfamily: stage III sporulation protein; stage III sporulation protein homology

Query Match 3.2%; Score 7; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SLSSASA 103

DB 222 SLSSASA 228

RESULT 30

T18788
hypothetical protein BE10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18788

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19022

A:Accession: T18788

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-301 <MTL>

A:Cross-references: UNIPROT:O17553; EMBL:Z93372; PIDN:CAB07546.1; GSPDB:GN00021; CESP:BE1

A:Experimental source: clone BE10

C:Genetics:

A:Gene: CESP:BE10.4

A:Map position: 3

A:introns: 87/3; 147/3; 210/3; 256/3

Query Match 3.2%; Score 7; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SLSSASA 103
DB 101 SLSSASA 107

Search completed: October 3, 2005, 11:46:49
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 3, 2005, 11:43:18 ; Search time 42 Seconds
(without alignments)
387.464 Million cell updates/sec

Title: US-10-694-978-2

Perfect score: 218
Sequence: 1 MSFVGENSGVKGSEDEWEDK.....IEFSPQPVCKAEMSPSEVSD 218

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	218	100.0	218	4 US-09-398-412B-2	Sequence 2, Appli
2	55	25.2	115	3 US-09-128-155-5	Sequence 5, Appli
3	55	25.2	115	3 US-09-128-155-9	Sequence 9, Appli
4	55	25.2	115	3 US-09-128-155-11	Sequence 13, Appli
5	55	25.2	136	3 US-09-128-155-11	Sequence 11, Appli
6	55	25.2	167	3 US-09-128-155-7	Sequence 7, Appli
7	55	25.2	178	3 US-09-128-155-2	Sequence 2, Appli
8	55	25.2	218	4 US-09-293-625-2	Sequence 4, Appli
9	55	25.2	218	4 US-09-398-412B-4	Sequence 4, Appli
10	48	22.0	63	3 US-09-128-155-4	Sequence 8, Appli
11	37	17.0	52	3 US-09-128-155-8	Sequence 12, Appli
12	28	12.8	185	3 US-09-128-155-18	Sequence 12, Appli
13	14	6.4	21	3 US-09-128-155-12	Sequence 12, Appli
14	8	3.7	559	4 US-09-364-206-47	Sequence 47, Appli
15	8	3.7	651	3 US-08-650-766-6	Sequence 6, Appli
16	8	3.7	651	3 US-08-922-635-5	Sequence 5, Appli
17	8	3.7	651	4 US-08-389-487-5	Sequence 6, Appli
18	8	3.7	1070	3 US-08-922-635-2	Sequence 22, Appli
19	8	3.7	1504	4 US-09-364-206-2	Sequence 2, Appli
20	8	3.7	1622	4 US-08-972-927-6	Sequence 6, Appli
21	7	3.2	73	4 US-09-107-532A-6620	Sequence 6620, Ap
22	7	3.2	108	4 US-09-513-999C-5928	Sequence 5928, Ap
23	7	3.2	148	4 US-09-640-211A-790	Sequence 790, App
24	7	3.2	204	4 US-09-710-279-3240	Sequence 3240, App
25	7	3.2	221	4 US-09-198-452A-292	Sequence 292, App
26	7	3.2	224	4 US-09-438-185A-281	Sequence 281, App
27	7	3.2	254	4 US-09-796-149B-4	Sequence 4, Appli

28	7	3.2	264	4 US-09-107-532A-7009	Sequence 7009, Ap
29	7	3.2	272	4 US-09-252-991A-22707	Sequence 22707, A
30	7	3.2	310	4 US-09-270-767-41004	Sequence 41004, A
31	7	3.2	310	4 US-09-270-767-56220	Sequence 56220, A
32	7	3.2	326	4 US-09-248-796A-19891	Sequence 19891, A
33	7	3.2	349	4 US-09-248-796A-14572	Sequence 14572, A
34	7	3.2	352	4 US-09-265-585C-116	Sequence 106, App
35	7	3.2	352	4 US-09-265-585C-115	Sequence 115, App
36	7	3.2	353	3 US-09-186-276B-32	Sequence 32, Appli
37	7	3.2	353	4 US-08-842-445-32	Sequence 32, Appli
38	7	3.2	353	4 US-09-186-188B-32	Sequence 32, Appli
39	7	3.2	353	4 US-09-265-585C-32	Sequence 32, Appli
40	7	3.2	377	2 US-08-969-106-6	Sequence 6, Appli
41	7	3.2	377	3 US-09-054-492B-1	Sequence 1, Appli
42	7	3.2	377	4 US-09-338-125-6	Sequence 6, Appli
43	7	3.2	382	3 US-09-134-001C-4483	Sequence 4483, Ap
44	7	3.2	398	4 US-09-328-352-6770	Sequence 6770, Ap
45	7	3.2	424	4 US-09-489-039A-9628	Sequence 9628, Ap
46	7	3.2	452	4 US-09-540-236-2370	Sequence 2370, Ap
47	7	3.2	469	4 US-09-328-352-6276	Sequence 6276, Ap
48	7	3.2	487	4 US-09-107-532A-5219	Sequence 5219, Ap
49	7	3.2	553	4 US-09-902-540-14945	Sequence 14945, A
50	7	3.2	744	4 US-09-328-352-7920	Sequence 7920, Ap
51	7	3.2	749	4 US-09-949-016-8645	Sequence 8645, Ap
52	7	3.2	749	4 US-09-949-016-8646	Sequence 8646, Ap
53	7	3.2	749	4 US-09-949-016-8647	Sequence 8647, Ap
54	7	3.2	749	4 US-09-949-016-8648	Sequence 8648, Ap
55	7	3.2	766	4 US-09-949-016-11355	Sequence 11355, A
56	7	3.2	766	4 US-09-949-016-11356	Sequence 11356, A
57	7	3.2	766	4 US-09-949-016-11357	Sequence 11357, A
58	7	3.2	766	4 US-09-949-016-11358	Sequence 11358, A
59	7	3.2	1054	4 US-09-626-301-2	Sequence 2, Appli
60	7	3.2	1054	4 US-08-340-428B-49	Sequence 49, Appli
61	7	3.2	1257	1 US-09-538-092-886	Sequence 886, App
62	7	3.2	1258	4 US-09-538-092-886	Sequence 886, App
63	7	3.2	1729	4 US-09-134-000C-5675	Sequence 57, Appli
64	6	2.8	25	3 US-09-049-691-57	Sequence 59, Appli
65	6	2.8	25	3 US-09-049-691-59	Sequence 62, Appli
66	6	2.8	25	3 US-09-049-691-62	Sequence 63, Appli
67	6	2.8	25	3 US-09-049-691-63	Sequence 63, Appli
68	6	2.8	39	4 US-09-270-767-34888	Sequence 34888, A
69	6	2.8	39	4 US-09-270-767-50105	Sequence 50105, A
70	6	2.8	43	4 US-09-674-973A-341	Sequence 341, App
71	6	2.8	44	4 US-09-674-973A-342	Sequence 342, App
72	6	2.8	47	4 US-09-902-540-13418	Sequence 13418, A
73	6	2.8	51	4 US-09-674-973A-345	Sequence 345, App
74	6	2.8	52	3 US-08-630-916A-71	Sequence 71, Appli
75	6	2.8	52	4 US-09-205-258-567	Sequence 567, App
76	6	2.8	52	4 US-09-674-973A-346	Sequence 346, App
77	6	2.8	60	4 US-09-328-352-7629	Sequence 7629, Ap
78	6	2.8	61	4 US-09-270-767-61868	Sequence 61868, A
79	6	2.8	62	4 US-09-270-767-40605	Sequence 40605, A
80	6	2.8	62	4 US-09-270-767-55821	Sequence 55821, A
81	6	2.8	62	4 US-09-248-796A-23629	Sequence 23629, A
82	6	2.8	63	4 US-09-543-681A-5842	Sequence 5842, Ap
83	6	2.8	67	2 US-08-588-258B-6	Sequence 6, Appli
84	6	2.8	67	3 US-08-460-505-6	Sequence 6, Appli
85	6	2.8	67	5 PCT-US96-08295-6	Sequence 6, Appli
86	6	2.8	70	4 US-09-270-767-33965	Sequence 33965, A
87	6	2.8	74	4 US-09-270-767-49182	Sequence 49182, A
88	6	2.8	74	4 US-09-248-796A-20872	Sequence 20872, A
89	6	2.8	75	4 US-09-489-039A-14009	Sequence 14009, A
90	6	2.8	75	4 US-09-270-767-40442	Sequence 40442, A
91	6	2.8	75	4 US-09-270-767-55658	Sequence 55658, A
92	6	2.8	78	4 US-09-489-039A-13889	Sequence 13889, A
93	6	2.8	78	4 US-09-134-000C-6521	Sequence 6321, Ap
94	6	2.8	78	4 US-09-583-110-3268	Sequence 2668, Ap
95	6	2.8	78	4 US-09-583-110-3268	Sequence 3202, Ap
96	6	2.8	79	4 US-09-304-615-167	Sequence 167, App
97	6	2.8	79	4 US-09-543-681A-6548	Sequence 6948, App
98	6	2.8	79	4 US-09-248-796A-26832	Sequence 26832, A
99	6	2.8	80	4 US-09-304-615-120	Sequence 120, App
100	6	2.8	81	4 US-09-543-681A-5027	Sequence 5027, App

```
101 6 2.8 82 4 US-09-621-976-5315 Sequence 5315, Ap
102 6 2.8 82 4 US-09-621-976-5321 Sequence 5321, Ap
103 6 2.8 84 4 US-09-107-433-4129 Sequence 4129, Ap
104 6 2.8 85 4 US-09-543-681A-8234 Sequence 8234, Ap
105 6 2.8 86 4 US-09-370-767-57072 Sequence 57072, A
106 6 2.8 87 4 US-09-248-796A-22328 Sequence 22328, A
107 6 2.8 88 4 US-09-489-039A-9865 Sequence 9865, Ap
108 6 2.8 91 1 US-08-455-896-8 Sequence 8, Appl1
109 6 2.8 91 2 US-08-933-149-8 Sequence 8, Appl1
110 6 2.8 91 2 US-09-082-343-8 Sequence 8, Appl1
111 6 2.8 91 3 US-09-082-253-8 Sequence 8, Appl1
112 6 2.8 91 4 US-08-987-505-1 Sequence 1, Appl1
113 6 2.8 91 4 US-09-162-622-8 Sequence 8, Appl1
114 6 2.8 91 4 US-09-509-015-8 Sequence 8, Appl1
115 6 2.8 91 4 US-09-270-767-39508 Sequence 39508, A
116 6 2.8 91 4 US-09-270-767-54725 Sequence 54725, A
117 6 2.8 91 5 PCT-US96-08235-8 Sequence 8, Appl1
118 6 2.8 93 4 US-09-248-796A-26322 Sequence 26322, A
119 6 2.8 94 4 US-09-949-016-10599 Sequence 10599, A
120 6 2.8 99 4 US-09-540-236-2992 Sequence 2992, Ap
121 6 2.8 100 4 US-09-513-999C-4593 Sequence 4593, Ap
122 6 2.8 104 4 US-09-513-999C-6549 Sequence 6549, Ap
123 6 2.8 105 4 US-09-583-110-4875 Sequence 4875, Ap
124 6 2.8 106 3 US-09-199-637A-283 Sequence 283, App
125 6 2.8 114 4 US-09-270-767-61594 Sequence 61594, A
126 6 2.8 113 4 US-09-513-999C-4899 Sequence 4899, Ap
127 6 2.8 114 1 US-08-040-548-4 Sequence 4, Appl1
128 6 2.8 114 1 US-08-466-344-4 Sequence 4, Appl1
129 6 2.8 115 4 US-09-248-796A-27123 Sequence 27123, A
130 6 2.8 118 4 US-09-765-815-8 Sequence 8, Appl1
131 6 2.8 118 4 US-09-311-021-158 Sequence 158, App
132 6 2.8 120 3 US-08-890-865A-14 Sequence 14, Appl1
133 6 2.8 120 4 US-09-621-976-5313 Sequence 5313, Ap
134 6 2.8 122 4 US-09-461-325-355 Sequence 355, App
135 6 2.8 122 4 US-10-012-542-355 Sequence 355, App
136 6 2.8 122 4 US-10-115-123-355 Sequence 355, App
137 6 2.8 122 4 US-09-902-540-11364 Sequence 11364, A
138 6 2.8 128 3 US-09-134-001C-3090 Sequence 3090, Ap
139 6 2.8 128 4 US-09-205-258-279 Sequence 279, App
140 6 2.8 128 4 US-09-270-767-31764 Sequence 31764, A
141 6 2.8 128 4 US-09-270-767-46981 Sequence 46981, A
142 6 2.8 131 1 US-08-409-731A-7 Sequence 7, Appl1
143 6 2.8 131 2 US-08-470-298B-7 Sequence 7, Appl1
144 6 2.8 132 2 US-08-470-298B-12 Sequence 12, Appl1
145 6 2.8 132 4 US-09-732-210-589 Sequence 589, App
146 6 2.8 132 4 US-09-732-210-590 Sequence 590, App
147 6 2.8 133 2 US-08-820-825-11 Sequence 11, Appl1
148 6 2.8 133 2 US-09-023-073A-7 Sequence 7, Appl1
149 6 2.8 133 3 US-09-307-817-11 Sequence 11, Appl1
150 6 2.8 133 3 US-09-361-737-7 Sequence 7, Appl1
```

ALIGNMENTS

```
RESULT 1
US-09-398-412B-2
; Sequence 2, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Tians, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reags
; TITLE OF INVENTION: methods
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398, 412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-398-412B-2
Query Match 100.0%; Score 218; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.1e-208;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVGENSVKMGSEDEWKEDEPOCCIEDPAGSPLEBGPSPPTMNVYHTRKYSINPKKF 60
Db 1 MSFVGENSVKMGSEDEWKEDEPOCCIEDPAGSPLEBGPSPPTMNVYHTRKYSINPKKF 60
QY 61 SHHDQHKVLVDSGNTLVDPDKNYRPIFPALASSLSASAEKGSILILGSKGFCL 120
Db 61 SHHDQHKVLVDSGNTLVDPDKNYRPIFPALASSLSASAEKGSILILGSKGFCL 120
QY 121 YCDKXGQSHPSLQTKKELMTLAAQKESARRPIFYRAQVGRNMLESAHPGFICT 180
Db 121 YCDKXGQSHPSLQTKKELMTLAAQKESARRPIFYRAQVGRNMLESAHPGFICT 180
QY 181 CNCNEPVGYTDKPENRKHIEFSFQPYCKAEMSPSEVSD 218
Db 181 CNCNEPVGYTDKPENRKHIEFSFQPYCKAEMSPSEVSD 218
```

```
RESULT 2
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5
```

```
Query Match 25.2%; Score 55; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.4e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 109 IILGVSKGFCLYCDKXGQSHPSLQTKKELMTLAAQKESARRPIFYRAQVGS 163
Db 6 IILGVSKGFCLYCDKXGQSHPSLQTKKELMTLAAQKESARRPIFYRAQVGS 60

RESULT 3
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
```

SEQ ID NO 9
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-9

Query Match 25.2%; Score 55; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.4e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 163
DB 6 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 60

RESULT 4
US-09-128-155-13
Sequence 13, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-13

Query Match 25.2%; Score 55; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.4e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 163
DB 6 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 60

RESULT 5
US-09-128-155-11
Sequence 11, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 136
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-11

Query Match 25.2%; Score 55; DB 3; Length 136;
Best Local Similarity 100.0%; Pred. No. 9.8e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 163
DB 27 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 81

RESULT 6
US-09-128-155-7
Sequence 7, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-7

Query Match 25.2%; Score 55; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 163
DB 58 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 112

RESULT 7
US-09-128-155-2
Sequence 2, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-2

Query Match 25.2%; Score 55; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 163
DB 69 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKMLAAQKESARRPFIYRAQVGS 123

RESULT 8
US-09-293-625-2
Sequence 2, Application US/09293625

```
/ Patent No. 6342371
/ GENERAL INFORMATION:
/ APPLICANT: Young, Peter R.
/ APPLICANT: McDONNELL, Peter C
/ TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
/ FILE REFERENCE: GP-70607
/ CURRENT APPLICATION NUMBER: US/09/293,625
/ CURRENT FILING DATE: 1999-04-16
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-293-625-2

Query Match      25.2%; Score 55; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQAQKESARRPFIYRAQVGS 163
109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQAQKESARRPFIYRAQVGS 163

RESULT 9
US-09-398-412B-4
/ Sequence 4, Application US/09398412B
/ Patent No. 6680380
/ GENERAL INFORMATION:
/ APPLICANT: Tilmans, Jacqueline C.
/ TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
/ FILE REFERENCE: DX0904K
/ CURRENT APPLICATION NUMBER: US/09/398,412B
/ CURRENT FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: US 60/100948
/ PRIOR FILING DATE: 1998-09-18
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 4
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-398-412B-4

Query Match      25.2%; Score 55; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQAQKESARRPFIYRAQVGS 163
109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQAQKESARRPFIYRAQVGS 163

RESULT 10
US-09-128-155-4
/ Sequence 4, Application US/09128155
/ Patent No. 6117654
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
/ FILE REFERENCE: 09404/052001
/ CURRENT APPLICATION NUMBER: US/09/128,155
/ CURRENT FILING DATE: 1998-08-03
/ EARLIER APPLICATION NUMBER: US 60/091,650
/ EARLIER FILING DATE: 1998-07-02
/ EARLIER APPLICATION NUMBER: US 60/054,646
/ EARLIER FILING DATE: 1997-08-04
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ US-09-128-155-4
```

```
/ LENGTH: 63
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-128-155-4

Query Match      22.0%; Score 48; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.3e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 MSPVGENSGVKKGSEDEKDEPQCCLEDPAGSPLEPGSLPTNNFVHT 48
1 MSPVGENSGVKKGSEDEKDEPQCCLEDPAGSPLEPGSLPTNNFVHT 48

RESULT 11
US-09-128-155-8
/ Sequence 8, Application US/09128155
/ Patent No. 6117654
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
/ FILE REFERENCE: 09404/052001
/ CURRENT APPLICATION NUMBER: US/09/128,155
/ CURRENT FILING DATE: 1998-08-03
/ EARLIER APPLICATION NUMBER: US 60/091,650
/ EARLIER FILING DATE: 1998-07-02
/ EARLIER APPLICATION NUMBER: US 60/054,646
/ EARLIER FILING DATE: 1997-08-04
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-128-155-8

Query Match      17.0%; Score 37; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      12 MGSEDEKDEPQCCLEDPAGSPLEPGSLPTNNFVHT 48
1 MGSEDEKDEPQCCLEDPAGSPLEPGSLPTNNFVHT 37

RESULT 12
US-09-128-155-18
/ Sequence 18, Application US/09128155
/ Patent No. 6117654
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
/ FILE REFERENCE: 09404/052001
/ CURRENT APPLICATION NUMBER: US/09/128,155
/ CURRENT FILING DATE: 1998-08-03
/ EARLIER APPLICATION NUMBER: US 60/091,650
/ EARLIER FILING DATE: 1998-07-02
/ EARLIER APPLICATION NUMBER: US 60/054,646
/ EARLIER FILING DATE: 1997-08-04
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 18
/ LENGTH: 185
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ NAME/KEY: synthetically generated
/ LOCATION: (1)...(185)
/ OTHER INFORMATION: human sequence predicted using an alignment algorithm which
/ OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
/ OTHER INFORMATION: interest in a stretch of genomic DNA
```

FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(185)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-128-155-18

Query Match 12.8%; Score 28; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 8.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCYCDKDGSHPSLOLK 136
Db 86 ILGVSKGEFCYCDKDGSHPSLOLK 113

RESULT 13
US-09-128-155-12
Sequence 12, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT FILING DATE: US/09/128,155
EARLIER FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PaetSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-12

Query Match 6.4%; Score 14; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 IFFALASSLSASA 103
Db 8 IFFALASSLSASA 21

RESULT 14
US-09-364-206-47
Sequence 47, Application US/09364206
Patent No. 6475752
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Baugh, Matthew R.
APPLICANT: Kaseer, Matthew R.
TITLE OF INVENTION: Mammalian Imidazole Receptor
FILE REFERENCE: PC-0006 US
CURRENT APPLICATION NUMBER: US/09/364,206
CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PERL Program
SEQ ID NO 47
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY:
OTHER INFORMATION: W43396
PUBLICATION INFORMATION:
US-09-364-206-47

Query Match 3.7%; Score 8; DB 4; Length 559;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100
Db 106 ALASSLS 113

RESULT 15
US-08-650-766-6
Sequence 6, Application US/08650766D
Patent No. 6015690
GENERAL INFORMATION:
APPLICANT: PILETZ, John E.
APPLICANT: IVANOV, Tina R.
TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
TITLE OF INVENTION: METHOD FOR CLONING THE SAME
FILE REFERENCE: Corrected Sequence Listing
Patent No. 6015690
CURRENT APPLICATION NUMBER: US/08/650,766D
CURRENT FILING DATE: 1996-05-20
EARLIER APPLICATION NUMBER: US 60/012,600
EARLIER FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 651
TYPE: PRT
ORGANISM: Homo sapiens
US-08-650-766-6

Query Match 3.7%; Score 8; DB 3; Length 651;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100
Db 106 ALASSLS 113

RESULT 16
US-08-922-635-5
Sequence 5, Application US/08922635A
Patent No. 6033871
GENERAL INFORMATION:
APPLICANT: PILETZ, John E.
APPLICANT: IVANOV, Tina R.
TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDAZOLINE RECEPTIVE POLYPEPTIDES
TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: Corrected Sequence Listing
Patent No. 6033871
CURRENT APPLICATION NUMBER: US/08/922,635A
CURRENT FILING DATE: 1997-09-03
EARLIER APPLICATION NUMBER: 08/650,766
EARLIER FILING DATE: 1996-05-20
EARLIER APPLICATION NUMBER: 60/012,600
EARLIER FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 651
TYPE: PRT
ORGANISM: Homo sapiens
US-08-922-635-5

Query Match 3.7%; Score 8; DB 3; Length 651;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100
Db 106 ALASSLS 113

```

RESULT 17
US-09-389-487-6
; Sequence 6, Application US/09389487
; Patent No. 6576742
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6576742
; CURRENT APPLICATION NUMBER: US/09/389,487
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: US 08/650,766
; EARLIER FILING DATE: 1996-05-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-389-487-6

Query Match      3.7%; Score 8; DB 4; Length 651;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 ALASSISS 100
Db      106 ALASSISS 113

RESULT 18
US-08-922-635-22
; Sequence 22, Application US/08922635A
; Patent No. 6033871
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6033871
; CURRENT APPLICATION NUMBER: US/08/922,635A
; CURRENT FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 08/650,766
; EARLIER FILING DATE: 1996-05-20
; EARLIER APPLICATION NUMBER: 60/012,600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-922-635-22

Query Match      3.7%; Score 8; DB 3; Length 1070;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 ALASSISS 100
Db      84 ALASSISS 91

RESULT 19
US-09-364-206-2
; Sequence 2, Application US/09364206
; Patent No. 6475752
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti

```

```

; APPLICANT: Tang, Y. Tom
; APPLICANT: Baugh, Matthew R.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: Mammalian Imidazoline Receptor
; FILE REFERENCE: PC-0006 US
; CURRENT APPLICATION NUMBER: US/09/364,206
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1504
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY:
; OTHER INFORMATION: 129581CD1
; PUBLICATION INFORMATION:
US-09-364-206-2

Query Match      3.7%; Score 8; DB 4; Length 1504;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 ALASSISS 100
Db      518 ALASSISS 525

RESULT 20
US-08-972-927-6
; Sequence 6, Application US/08972927
; Patent No. 6166290
; GENERAL INFORMATION:
; APPLICANT: Rea, Philip A
; APPLICANT: Lu, Yu-ping
; APPLICANT: Li, Ze-Sheng
; TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: One Commerce Square, 2005 Market Street, 22nd
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: US
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,927
; FILING DATE: 18-NOV-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,040
; FILING DATE: 18-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/061,328
; FILING DATE: 08-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Doyle Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-1202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 amino acids

```

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-972-927-6

Query Match 3.7%; Score 8; DB 3; Length 1622;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 KVLVDSG 75
DB 1440 KVLVDSG 1447

RESULT 21
US-09-107-532A-6620
Sequence 6620, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 6620:
SEQUENCE CHARACTERISTICS:

LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...73
SEQUENCE DESCRIPTION: SEQ ID NO: 6620:
US-09-107-532A-6620

Query Match 3.2%; Score 7; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 SSLSAS 102
DB 39 SSLSAS 45

RESULT 22
US-09-513-999C-5928
Sequence 5928, Application US/09513999C
Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 6783961
FILE REFERENCE: 59 US2,REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5928
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-5928

Query Match 3.2%; Score 7; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DSGNLIA 79
DB 31 DSGNLIA 37

RESULT 23
US-09-640-211A-790
Sequence 790, Application US/09640211A
Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021CIU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: PatsSeq for Windows Version 4.0
SEQ ID NO 790
LENGTH: 148
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-640-211A-790

Query Match 3.2%; Score 7; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 ASSLSA 101
DB 20 ASSLSA 26

RESULT 24
US-09-710-279-3240
Sequence 3240, Application US/09710279
Patent No. 6703492

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: F03480US

; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3240
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-3240

Query Match 3.2%; Score 7; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 KVKSLNP 57
|||
Db 82 KVKSLNP 88

RESULT 25
US-09-198-452A-292
; Sequence 292, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 292
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-292

Query Match 3.2%; Score 7; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KSLNPKK 59
|||
Db 44 KSLNPKK 50

RESULT 26
US-09-438-185A-281
; Sequence 281, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Davis, Sue
; APPLICANT: Kaiman, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281

; LENGTH: 224
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0279
US-09-438-185A-281

Query Match 3.2%; Score 7; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KSLNPKK 59
|||
Db 47 KSLNPKK 53

RESULT 27
US-09-796-149B-4
; Sequence 4, Application US/09796149B
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-313424/USC
; CURRENT APPLICATION NUMBER: US/09/796,149B
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149B-4

Query Match 3.2%; Score 7; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 FALASSL 98
|||
Db 27 FALASSL 33

RESULT 28
US-09-107-532A-7009
; Sequence 7009, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 7009:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 264 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1..264
 SEQUENCE DESCRIPTION: SEQ ID NO: 7009:
 US-09-107-532A-7009

Query Match 3.2%; Score 7; DB 4; Length 264;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 QLKKEKL 140
 Db 251 QLKKEKL 257

RESULT 29
 US-09-252-991A-22707
 ; Sequence 22707, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 22707
 ; LENGTH: 272
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-22707

Query Match 3.2%; Score 7; DB 4; Length 272;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 VLVLDSG 75
 Db 14 VLVLDSG 20

RESULT 30
 US-09-270-767-41004
 ; Sequence 41004, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 41004
 ; LENGTH: 310
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-41004

Query Match 3.2%; Score 7; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 LILUGVS 114
 Db 195 LILUGVS 201

Search completed: October 3, 2005, 11:47:36
 Job time : 45 secs

THIS PAGE BLANK (USPTO)